In the Claims:

Please amend the claims as shown in the following listing of claims, which will replace all prior versions and listings of claims in the application.

1-66. (Canceled)

67. (New) A method of treating an ACE2 decreased state comprising administering to a mammal having an ACE2 decreased state a therapeutically effective amount of an ACE2 agonist, activator, or a transgene coding ACE2.

68. (New) The method of claim 67, wherein the mammal is a human.

69. (New) The method of claim 67, wherein the decreased ACE2 state is associated with hypertension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, arteriosclerosis, renal failure, and/or lung disease.

70. (New) The method of claim 67, further defined as a method of gene therapy for an ACE2-decreased state, comprising administering an effective amount of a transgene coding ACE2 to an organ of a patient.

71. (New) The method of claim 70, wherein the affected organ is the heart or kidney or lung or blood vessels.

72. (New) The method of claim 70, wherein the ACE2 transgene is administered to the patient in a gene therapy vector.

73. (New) The method of claim 67, further comprising administering to the mammal an effective amount of an ACE2 activator, wherein the ACE2 activator is co-administered with an ACE inhibitor.

74. (New) A polynucleotide comprising a sequence which binds specifically to a region upstream or downstream of an ACE2 nucleic coding region wherein the region is proximate to a nucleotide polymorphism that decreases ACE2 expression.

75. (New) The polynucleotide of claim 74, comprising 8 to 10, 8 to 15, 8 to 20, 8 to 25, 25, 25 to 50, 50 to 75, 50 to 100, 100 to 200, 200 to 500, or 500 to 1000 nucleotides.

76. (New) The polynucleotide of claim 74, wherein the nucleic acid specifically binds proximate to one of ACE2a-ACE2m under high stringency hybridization conditions.

77. (New) The polynucleotide of claim 76, wherein the stringent hybridization conditions comprise 0.1XSSC, 0.1% SDS at 65°C.

78. (New) The polynucleotide of claim 74, further defined as comprising a sequence complementary to an ACE2 polymorphism.

79. (New) The polynucleotide of claim 78, further defined as comprising a sequence of:

(a) 8-50 nucleotides of an upstream or downstream region of ACE2 which is proximate to a nucleotide polymorphism, wherein the sequence includes one of ACE2a-ACE2m and comprises all or part of one of the sequences in Figure 11;

(b) a sequence that is complementary to a sequence specified in (a); or

c) a sequence having at least 70% sequence identity to a sequence in (a) or (b) and capable of hybridization to ACE2 under high stringency hybridization conditions.

80. (New) The polynucleotide of claim 74, further defined as a hybridization assay probe.

81. (New) The polynucleotide of claim 80, further defined as detectably labeled.

82. (New) The polynucleotide of claim 81, wherein the detectable label comprises a fluorogenic dye, a biotinylation modification, and/or a radiolabel.

83. (New) A method of ACE2 genotyping an animal comprising:

obtaining an ACE2 nucleic acid sample derived from the animal including regions upstream and downstream of the ACE2 coding region; and

detecting a region of an ACE2 nucleic acid that includes an ACE2 single nucleotide polymorphism in the nucleic acid sample.

84. (New) The method of claim 83, wherein the polymorphism reduces ACE2 expression compared to wild type ACE2.

85. (New) The method of claim 83, wherein the nucleotide polymorphism is one of ACE2a-ACE2m.

86. (New) The method of claim 85, further comprising determining whether the animal is homozygous or heterozygous for the ACE2 polymorphism.

87. (New) The method of claim 86, wherein the animal is a human and the ACE2 genotype is used to determine if the human has or is at risk of an ACE2 decreased state disease.

88. (New) The method of claim 87, wherein the disease comprises cardiovascular disease, kidney disease, lung disease, and/or affects blood vessels.

89. (New) The method of claim 88, wherein the disease is further defined as hypertension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, arteriosclerosis, or renal failure.

90. (New) The method of claim 83, wherein the nucleic acid is obtained by amplifying the nucleic acid from the animal.

91. (New) The method of claim 90, wherein the nucleic acid is obtained by amplification with all or part of a polynucleotide comprising a sequence which binds specifically to a region upstream or downstream of an ACE2 nucleic acid coding region wherein the region is proximate to a nucleotide polymorphism that decreases ACE2 expression.

92. (New) The method of claim 83, wherein detecting comprises determining the nucleotide sequence of the ACE2 nucleic acid.

93. (New) The method of claim 83, wherein detecting comprises contacting, under high stringency conditions, the nucleic acid with a polynucleotide comprising a sequence which binds specifically to a region upstream or downstream of an ACE2 nucleic acid coding region wherein the region is proximate to a nucleotide polymorphism that decreases ACE2 expression.

94. (New) The method of claim 93, wherein the polynucleotide will selectively hybridize proximate to a region of ACE2 nucleic acid that comprises a single polymorphism distinctive of an ACE2 polymorphism.

95. (New) The method of claim 83, wherein detecting comprises:

performing a restriction endonuclease digestion of the nucleic acid, thereby providing a nucleic acid digest; and

contacting the digest with the polynucleotide.

96. (New) The method of claim 95, wherein the hybridization occurs either during or subsequent to PCR amplification and the analysis is by "Real-Time" PCR analysis or fluorimetric analysis.

97. (New) The method of claim 95, wherein detect includes size analysis of the nucleic acid.